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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

RESULT AAA38006

AAA38006 standard; cDNA; 534 BP.

AAA38006;

UCK-1 nucleotide sequence 22-AUG-2000 (first entry) a a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
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Chemotaxic factor useful for treatment and diagnosis of immunocyte disorders - has immunocyte chemotaxic stimulating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                          P-PSDB; AAY98142.
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            ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy; transgenic animal; Alzheimer's disease; Parkinson's disease; burn; amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia; ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
      utcer; osteoporosis; bone degenerative disorder; gut protection; lung; liver fibrosis; immune def
                                                                               Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
                                                                                                            cDNA encoding novel human secretory protein, Seq ID No 13.
                                                                                                                                                      18-DEC-2001 (first entry)
                                                                                                                                                                                                                      AAS44932 standard; cDNA; 655 BP
                                                                                                                                                                                                                                                                                                           481
                                                                                                                                                                                                                                                                                                            This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis activity and a haemopoiesis stimulating effect. The invention relates to UCK proteins, their encoding nucleotide sequences and antibodies and antagonists against the proteins. The nucleotide and protein sequences are useful for the preparation of a composition for the diagnosis and treatment of diseases associated with abnormal immunocyte function and low haemopoiesis function caused by radiotherapy and chemotherapy used to
                                                                                                                                                                                                                                                                                                                                                                           421
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fibrosis; immune deficiency; infection;
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No. 3.5e-107;
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CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is convolved in increasing haematopolesis, stem cell survival, bone growth comprehensing transgenic animals useful for studying the in vivo activities of creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of (II) is also useful for coreating transgenic animals useful for studying the in vivo activities of (I) induces the proliferation of neural cells and regeneration of nerve can brain nervous system diseases and neuropathles, such as Alzheimer's, and brain tissue and is useful for the treatment of central and corporation of nerve cativity, regulation of haematopolesis and is useful for treating myeloid and for regeneration of haematopolesis and is useful for treating myeloid and for regeneration of bone, cartilage, tendon, ligament and/or nerve concerns, for treating osteoporosis, osteoarthrits, bone degenerative ulcers, for treating osteoporosis, osteoarthrits, bone degenerative culcers, for treating osteoporosis, osteoarthrits, bone degenerative culcers, or periodontal disease. Furthermore, (I) is also useful for caperiusion injury in various tissues, various immune deficiencies and conditions, such as asthma or other respiratory problems. CC disorders including severe combined immunodeficiency (SCID), bacterial or reactions and conditions, such as asthma or other respiratory problems. CC distary fat, lipid, protein, carabolism, anabolism, storage or elimination of canalgesic effects or other pain reducing effects, immunoglobulin like an antigen in a vaccine composition to raise an antigen in the contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 13; 107pp; English.
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19-MAY-2000;
17-JUN-2000;
14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel isolated human secreted polypeptides (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer, neurological, inflammatory, and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAU28032
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Zhang J, Chen R,
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Matches 507;

Conservative

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Mismatches

Local Similarity

94.9%;

Score 507; Pred. No.

DB 22; .7e-101;

Length 655;

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Sequence

655

BP;

178

A; 129 C; 181 G; 167 T;

0 other;

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15-SEP-2000;
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 P-PSDB; AAM23856
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                                                                          (HYSE-) HYSEQ INC.
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              2001-476164/51.
                                        Drmanac RA,
                                                   Liu C,
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2000US-0631451.
2000US-0663870.
                                                   Zhou P,
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g J, Werhm
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man T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 451; 1275pp; English.
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                                                                                                                                                                                                                                                                                                                                                                            TIGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGCCCCTTA 144
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Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.

norse;

Human EST-derived coding sequence SEQ ID NO: 405.

12-OCT-2001 (first entry)

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                                                        143
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                                                                                                203 TIGGIGGAGGGGTGTITGCACTIGIGACAGCAGTAIGCTGICTIGCCGACGGGGCCCTIA 144
                                                                                                                                                     263 CAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCACAACATTGACAG
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                                                                                                                                                                                                                                                                                                                443 ATCCCTTCCCAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTG
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                                                                                                                                                                                                                                                                                                                                                                    503 GGGAAGCCGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, diagnostics, raising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                75 atcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctgctg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                         TTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAAGCCCTGTGCATGAAA
                                                        tttaccggaagcttctgttcaatcccagcggtccttaccagaaaaagcctgtgcatgaaa 434
                                                                                                                tt99t99ag99gtgtttgcacttgtgacagcagtatgctgtcttgccgacggggccctta
                                                                                                                                                                   cagtattcatgctcatcgtatctgtgttggcactgataccagaaaccaccacaacattgacag
                                                                                                                                                                                                         TCAGTGTGAAAGGCCACGTGAAGATGCTGCGGCTGGATATTATCAACTCACTGGTAACAA
                                                                                                                                                                                                                          tcagtgtgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaacaa 254
                                                                                                                                                                                                                                                              CTGGGTCTGCAGACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCT
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99.4%;
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Pred. No. 2.1e-99;
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В QΥ

Query Match Best Local :

Matches

499;

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Similarity

93.1%; 98.4%;

Score 497.2; DB 2 Pred. No. 3.6e-99; Mismatches

DB 22; 6.

Indels Length 558;

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                                                                                 cancer associated nucleic acid molecules (N) and proteins (P), where cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, expression. For example, N and P may be used in the prevention, expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing or deletions in a patient's genome that affect the activity of P by expressing the nucleic acids into a host cell and culturing the cell and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 present invention
Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;
                           present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 3428; 9803pp; English.
                                                                                                                                                                                                                                                                                             AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAG75430.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-2001
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RESULT
AAA87730
ID AAA8
XX AAA8
AC AAA8
AC AAA8
XX 28-N
DT 28-N
XX Hume
KW Chrc
KW Chrc
KW Ineu
KW mitc
KW mitc
XX Home
XX Home
XX Sept
XX 29-\
YX 20-\
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YX WPI
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                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome mapping; cancer; autoimmune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; forensic procedure; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein encoding cDNA SEQ ID #29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-2000
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                                                                                                                                                                                                                                                                                                   WO200037491-A2.
                 Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                 22-DEC-1998;
25-JUN-1999;
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                                                                   P-PSDB; AAB25768
                                                                                                                   Bougueleret L,
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                                                                                                                                                                                                                                                                                                                                                                 shock;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents human cDNA encoding a secreted protein. The invention relates to sequences AAA87725-A87774 which encode human secreted proteins AAB87763-B25812. The proteins include signal peptides. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins. Also contained in the invention are methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, gene
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                                                                                                                                                                                                                                                                                                                                                                                                    tcagtgtgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgggtctgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgct 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gggaagccgagctgggcgagaagtaggggagggcggtgctccg-cgcggtggcngttgct
tttaccggaagcttctgttcaatcccagcggtccttaccagaaaaagcctgtgcatgaaa
                                                                                                                                                                                                                                                                                                        cagtattcatgctcatcgtatctgtgttggcactgataccagaaaccacaacattgacag
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                                                                                            aaaaagaagttttgtaattttatattactttttagtttgatactaagtattaaacatatt
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                                                                        aaaaagaagttttgtaattttatattactttttagtttgatactaagtattaaacatatt
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05-APR-2001 (first entry)

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to 49 Secreted proteins and the encoding them. The protein and nucleic acids may be used in the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 Secreted proteins and the nucleic acids encoding gene therapy and for detecting similar sequences in
       427
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21-DEC-1999;
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23-MAY-1997;
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23-MAY-1997;
23-MAY-1997;
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970S-0043312

970S-0043313

970S-0043568

970S-0043576

970S-0043576

970S-0043570

970S-0043671

970S-0043672

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970S-0047501

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18-AUG-1997
22-AUG-1997
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06-JUN-1997;
06-JUN-1997;
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                                                                                Kyaw H,
                                                     NPI; 1998-506364/43.
                                                                 H, Lafleur DW, Li Y, Rucci
Shi Y, Soppet DR, Young PE,
                                              AAW74818.
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97US-0051926.
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970S-0047613.

970S-0047614.

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970S-0047632.

970S-0047633.

970S-0048964.
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97US-0056876.
97US-0056877.
97US-0056878.
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97US-0058785.
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Brewer LA, Carter KC, Duan R, Ebner K, ie AM, Fischer CL, Florence KA, Greene JM eur DW, Li Y, Moore PA, Ni J, Olsen HS, Y, Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                    Ebner R,
            Greene JM, Huger CA;
                                                                         Endress GA;
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New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Human; secreted protein; fusion protein; gene therapy; protein therapy;

Human secreted protein gene 88 clone HAUAV32.

19-JAN-1999 (first entry)

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23 MAY -1997

23 MAY -1997
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11-APR-1997;
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07-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic; shock; Alzheimer's disease; restenosis; AIDS; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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970S-0043312

970S-0043313

970S-0043568

970S-0043568

970S-0043569

970S-0043670

970S-0043670

970S-0047602

970S-0047501

970S-0047501

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970S-0047613

970S-0047615

970S-0047615
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97US-0040626.
97US-0043311.
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18-AUG-1997
22-AUG-1997
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13-JUN-1997;
08-JUL-1997;
16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                97US-0056894.
97US-0056903.
97US-0056908.
97US-0056910.
97US-0056911.
97US-0057650.
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970S-0056845

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97US-0056889.
97US-0056892.
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97US-0049610.
97US-0051926.
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97US-0056631
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Feng P, Kyaw H, P-PSDB; Ruben 1998-506364/43. DB; AAW74961. , MS Lafleur DW, I, Shi Y, So Ferrie AM, Brewer r LA, Carter KC, Duan R, Ebner R, E Fischer CL, Florence KA, Greene JM, 1, Li Y, Moore PA, Ni J, Olsen HS, Soppet DR, Young PE, Yu GL, Zeng Z; Soppet DR, (A, Greene JM, Hu JS; GA;

This sequence represents a nucleic acid molecule designated Gene 88 from the human cDNA clone HAUAV32 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions e.g. by protein or gene therapy. Also, pathological polypeptides in a sample or by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 nor unicleotides. Specific uses are described for each of the 186 nor unicleotides. Claim 1; Page 472; 721pp; English. New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

they are most highly expressed in

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AAX97826
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                                04-SEP-1998;
13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
                                                                                                                                                                Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic; diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
                                                                                                                                                                                                                        23-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                   AAX97826 standard; cDNA; 500
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Local Similarity 97.4%;
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                                  98US-0099273.
97US-0066677.
97US-0069957.
  98US-0074121.
98US-0081563.
98US-0096116.
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Pred. No. 3.9e-95;
                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAY36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies cappeable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. Uses also include design of expression vectors and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 500 BP; 135 A; 102 C; 125 G; 129 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extended cDNAs encoding secreted proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                Human protein clone HP10357 full length coding sequence.
                                                                              AAA15929 standard; cDNA; 467
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                           12-JUN-2000 (first entry)
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97.8%;
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Pred. No. 1.4e-92;
4; Mismatches 5; Indels 2;
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301 320 241 260

500 481

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cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; osteoporosis; osteoarthritis; periodontal disease; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury; systemic cytokine damage; tissue differentiation; contraceptive; stroke; septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
nephritis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein; hydrophobic domain; nutritional source; haematopoiesis;
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WO200005367-A2
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03-FEB-2000

99WO-JP03929.

29-SEP-1998; 25~AUG-1998; 09-SEP-1998; 24-JUL-1998; 07-AUG-1998; 98JP-0275505 98JP-0254736 98JP-0224105. 98JP-0238116. 98JP-0208820.

SAGAMI CHEM RES CENT PROTEGENE INC

Kato S, Kimura T;

AAY94861

Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke

Claim 4; Page 228; 351pp; English.

CC infections diseases caused by viral, bacterial, fungal or other CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid CC arthritis. It is also used in immune suppression after organ CC arthritis. It is also useful in the treatment of allergic reactions and CC conditions such as asthma, and in immune suppression after organ CC and consequently in the treatment of myeloid or lymphoid cell CC regeneration. The protein is useful in regulation of haematopoiesis CC deficiencies. It is also used in compositions for tissue growth or CC regeneration. The protein is also used in the treatment of seteoporosis consequently in the treatment of myeloid or lymphoid cell cor osteoarthritis and in the treatment of periodontal disease and other system disorders such as Alzheimer's disease, Parkinson's disease, and CC treatment of lung or liver fibrosis, reperfusion injury in various consequent of lung or inhibiting tissue differentiation. They are calso used for promoting or inhibiting tissue differentiation. They are calso used for promoting or inhibiting tissue differentiation. They are calvities and as a fertility inducing therapeutic. They are used for conditions resulting from systemic cytokine damage. They are calvities and as a fertility inducing therapeutic. They are used for conditions resulting from coagulation activities e.g. myocardial confirmation or stroke. They also acts as receptors, receptor ligands or treat inflammatory conditions such as septic shock, sepsis, ischaemia nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activities and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat information. genetic marker. The protein can also be used as a marker, and to identify potential genetic disorders. The DNA and protein can also be used as This sequence encodes a human protein of the invention, which has hydrophobic domains. The DNA sequences can be used as a probe or as a

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RESULT 1
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                                09-FEB-1998;
13-APR-1998;
10-AUG-1998;
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                                                                    04-SEP-1998;
13-NOV-1997;
17-DEC-1997;
        (GEST ) GENSET
                                                                                                                      13-NOV-1998;
                                                                                                                                                27-MAY-1999
                                                                                                                                                                                                               Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic; diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
                                                                                                                                                                                                                                                       Human secreted protein encoding cDNA #61.
                                                                                                                                                                                                                                                                                   23-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                   AAX97873 standard; cDNA; 413
                                                                                                                                                                                                                                                                                                                                                                                           421 ttactttttagtttgatactaagtattaaacatatttctgtattctt 467
                                                                                                                                                                                                                                                                                                                                                                                                           459 ttactttttagtttgatactaagtattaaacatatttctgtattctt 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 467 BP; 118 A; 101 C; 121 G; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reperfusion injury, arthritis, and nephritis. They can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 acgtgcagccgaaaataaaacatcgccccttctgcttcagtgtaaaggccacgtgaaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 cagccagctgagaagagttgagggaaagtgctgctgctgggtctgcagacgcgatggata 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 cagccagctgagaagagttgagggaaagtgctgctgctggggtctgcagacgcgatggata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 aggggagggcggtgctccgccgcggttggcggtttgctatcgcttcgcagaacctactcagg 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 aggggagggcggtgctccgccgcggtggcggttgctatcgcttcgcagaacctactcagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                        ccageggteettaccageaaaageetgtgeatgaaaaaaaagaagttttgtaattttata
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgacagcagtatgctgtcttgccgacggggcccttatttaccggaagcttctgttcaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgacagcagtatgctgtcttgccgacggggcccttatttaccggaagcttctgttcaatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tgttggcactgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgctgcggctggatattatcaactcactggtaacaacagtattcatgctcatcgtatctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgttggcactgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgctgcggctggatattatcaactcactggtaacaacagtattcatgctcatcgtatctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acgtgcagccgaaaataaaacatcgccccttctgcttcagtgtgaaaggccacgtgaaga 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                            98US-0074121
98US-0081563
                                98US-0096116
                                                                                            98US-0099273
                                                                                                                    98WO-IB01862
                                                                    97us-0069957
                                                                                 97us-0066677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.2%;
99.8%;
                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 465.4; DB 2
Pred. No. 2.9e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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RESULT 13
AACO0147
ID AACO01.
XX
AC AACO01.
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AAX97813-X97906 represent extended cDNA's which encode novel human secreted proteins (see AAX36129-Y36222) and which have cytostatic, thrombotic and osteopathic activity. The extended cDNAs can be used to express secreted proteins or parts of them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, foreisic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 261; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Extended cDNAs encoding secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY36189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic, forensic, gene therapy and chromosome mapping procedures uses also include design of expression vectors and secretion vectors
                                                                                                                                                                                                                                                              AAC00147 standard; cDNA; 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
 21-FEB-2000; 2000EP-0200610
                                06-SEP-2000
                                                                                                                                                                    Human secreted protein 5' EST, SEQ ID NO: 145.
                                                                                                                                                                                                  06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                             EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                      407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            госат
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgagaaqagttgagggaaagtgctgctgctggggtctgcagacgcgatggataacgtgcag 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gtatgctgccttgccgacggggcccttatttaccggaagcttctgttcaatcccagcggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtgacagca 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ctggatattatcaactcactggtaacaacagtattcatgctcatcgtatctgtgttggca 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccgaaaataaaacatcgccccttctgcttcagtgtgaaaggccacgtgaagatgctgcgg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccgaaaataaaacatcgccccttctgcttcagtgtgaaaggccacgtgaagatgctgcgg 226
                                                                                                                                                                                                                                                                                                                                                                                                ccttaccagaaaaagcctgtgcatgaaaaaaaagaagttttgtaattttatattactttt
                                                                                                                                                                                                                                                                                                                                                                                                                              ccttaccagaaaaagcctgtgcatgaaaaaaaagaagttttgtaattttatattacttt 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtatgctgtcttgccgacggggcccttatttaccggaagcttctgttcaatcccagcggt 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctgataccagaaaccacaacattgacagttggtggaggggtgttttgcacttgtgacagca 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctggatattatcaactcactggtaacaacagtattcatgctcatcgtatctgtgttggca
                                                                                                                                                                                                                                                                                                                                       412;
                                                                                                                       therapy; chromosome mapping; ss
                                                                                                                                     5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 411.4; DB 2
Pred. No. 1.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; Length 413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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AAZ34051 RESULT

14

AAZ34051 standard; cDNA; 663 BP

369 tttaccggaagcttctgttcaatcccagcggtccttaccagaaaaag

415

AAZ34051;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length constant of the sequence of the sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID 145; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 415 BP; 101 A; 97 C; 126 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                129
                                                                                                                                                                                                                                                                                                                       189
                                                                                                                                                                                                                                                                                                                                                                             195
                                                                              309 ttggtggaggggtgtttgcacttgtgacagcagtatgctgtcttgccgacggggccctta 368
                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 gtgaagccgagctgggcgagaagtaggggaggaggtgctccgccgcggtggcggttgct 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 atcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 gggaagccgagctgggcgagaagtaggggagggcggtgctccgccgcggtggcggttgct
                                                                                                                                                                                                                                                                                                                                                                                                                       cagtattcatgctcatcgtatctgtgttggcactgataccagaaaccacaacattgacag
                                                                                                                                                                                                                                                                                                                                            tcagtgtgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaacaa 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctg
                                                                                                                                                                                                                            cagtattcatgetcatcgtatctgtgttggcactgataccagaaaccacaacattgacag 314
tttaccggaagcttctgttcaatcccagcggtccttaccagaaaaag 421
                                                                                                                                                                                                                                                                                                              tcagtgtgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaacaa
                                                                                                            ttggtggaggggtgtttgcacttgtgacagcagtatgctgtcttgccgacggggccctta 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG00141.
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99.8%;
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Pred. No. 3.2e-79;
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07-DEC-1999 (first entry)

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01-APR-1998
01-APR-1998
01-APR-1998
01-APR-1998
08-APR-1998
08-APR-1998
09-APR-1998
09-APR-1998
15-APR-1998
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21-APR-1998
22-APR-1998
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29-APR-1998
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20-MAR 1998
20-MAR 1998
20-MAR 1998
20-MAR 1998
25-MAR 1998
26-MAR 1998
27-MAR 1998
27-MAR 1998
27-MAR 1998
27-MAR 1998
27-MAR 1998
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11-MAR-1998;
12-MAR-1998;
12-MAR-1998;
13-MAR-1998;
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31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-1998;
11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PR0772 nucleotide sequence.
    98US-0081071

98US-00811071

98US-0081203

98US-0081817

98US-00818183

98US-0081952

98US-0082568

98US-0082568

98US-0082704

98US-0083336

98US-0083496

98US-0083496

98US-0083545

98US-0083554

98US-0083558
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98US-0079786.
98US-0079920.
98US-0079923.
98US-0080105.
98US-0080107.
98US-0080107.
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98US-0079656.
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98US-0078939.
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98US-0078886
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밁 QΥ 밁 Qy

61

142 tgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgcttcagtgt 201

cgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctgctgggtc cgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctgctggtgctgct

60

Matches 504;

Conservative

0; Mismatches Score 335; DB 20; Pred. No. 7.4e-64;

0; Indels 159; Gaps Length 663;

1;

Query Match Best Local Similarity

62.7%;

DB 20;

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The present invention describes secreted and transmembrane polypeptides and their polypucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ4338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                         13-MAY-1998
13-MAY-1998
15-MAY-1998
15-MAY-1998
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25-MAY-1998
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28-MAY-1998
28-MAY-1998
                                                                                                                                                       Claim 2; Fig 69; 530pp; English.
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06-MAY-1998;
06-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
                                                                                                                                                                                 adhesion disorders
                                                                                                                                                                                   New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular
                                                                                                                                                                                                                                                           Wood WI,
                                                                                                                                                                                                                            WPI; 1999-551358/46.
P-PSDB; AAY41713.
                                                                                                                                                                                                                                                                               (GETH ) GENERTECH INC.
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98US-0086023
98US-00864392
98US-0086430
98US-0086486
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26-JUL-1999
29-CCT-1999
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                                                                                                                                                                                               WO200053756-A2
                                                                                                                                                                                                                                            expressed sequence tag; detection; cancer; ss
                                                                                                                                                                                                                                                      Human; secreted protein; transmembrane protein; PRO;
                                                                                                                                                                                                                                                                             Human PRO772 (UNQ410) nucleotide sequence SEQ ID NO:189.
                                                                                                                                                                                                                                                                                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                 AAC78498 standard; cDNA; 663 BP
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                                                                                                                                                   2000WO-US04341
99US-0145698.
99US-0162506.
99WO-US28313.
99WO-US28551.
99WO-US28565.
                                                        99US-0131445.
99US-0134287.
99US-0141037.
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99US-0123957
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                                                                                                                                                                                                                                                           EST; cytostatic;
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attttcatacttttatatgtactcagacttgatcgattaatgaagtggttattttggcc

283 ggcactgataccagaaaccacaacattgacagttggtggagggggtgtttgcacttgtgac

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Best Local Similarity
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30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating blological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;
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Kljavin IJ,
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                              catcycacaaycccctgaaccatatattyttatcactygatttyaaytcaccyttatctt
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Filvaroff E,
Godowski PJ,
Kuo SS, Nap
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2000WO-US00277.
2000WO-US00376.
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99WO-US31243.
99WO-US31274.
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76.0%;
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E, Fong S, Gao W, Gerber H, Gerritse
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napher MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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Search completed: July 17, 2002, 09:23:34 Job time: 9644 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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US-08-545-1968-10
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US-08-865-297-5
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US-07-867-106-2
5168051-9
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US-09-448-076-1
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  US-08-980-060-3
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                                                                                                                                                                                    Patent No. 5219739
Patent No. 5219739
Sequence 1, Appli
Sequence 1, Appli
Sequence 35, Appl
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sequence 2, Appli
patent No. 5194596
patent No. 5219739
                                                                                                                                                                                                                                                                                                               Description
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Sequence 12,
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patent No. 5168051
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                                                                              346 agtatgotgtottgoogaoggggcocttatttacoggaagottotgttoaatoocagogg 405
                                                                                                             103 actgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtgacagc 162
                                                                                                                      286 actgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtgacagc 345
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                                                                                                                                                                                                               Local Similarity
                             223
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                                                                     agtatgctgtcttgccgacggggcccttatttaccggaagcttctgttcaatcccagcgg
                          tccttaccagaaaaagcctgtgcatgaaaaaaaaagaagttttgtaattttatattactt 282
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Result NO.

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7.5	7.6	7.6	7.6	7.7.	7 7 . 6	7.6	7.7.	7.6
770 817	2007 2217	2007	1881	1472	1472 1472	1253 1472	2444 2625	1046
44	4 4	ω 4	<i>-</i> 4- ω	4 4	44	2 4	+ω 4	- 4
US-09-385-982-542 US-08-885-469-1	US-09-005-051-38 US-09-244-314-1	US-08-747-221B-38 US-09-005-051-36	US-08-874-102-48 US-08-747-221B-36	US-08-874-102-12 US-08-874-102-46	US-08-781-420-12 US-08-874-102-10	US-08-591-629-1 US-08-781-420-10	US-08-906-791-1 US-09-245-041-18	US-08-484-332C-4 rrs-08-451-405A-2
1, 1	1, 1	Sequence 36, Appl Sequence 36, Appl	30,	Sequence 46, Appl	10,	Sequence 10, Appl	Sequence 1, Appl Sequence 18, Appl	2,4

ALIGNMENTS

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Sequence 95, Application US/09385982

Sequence 95, Application US/09385982

Patent No. 6262334

GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
TITLE OF INVENTION UNMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
OTHER INFORMATION: n = A,T,C
US-09-385-982-95
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version
                                                                            NAME/KEY: misc_feature LOCATION: (1)...(392)
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50.9%; 95.5%;

0; Mismatches

Score 272; DB 4; Pred. No. 8.4e-61;

DB 4; Length 392; 12;

Indels

2;

Gaps

2

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US-08-545-196B-12
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GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
                                                                                     Sequence 12, Application US/08545196B
Part No. 6080577
                                                                                                                                                                                                                                                                                                                                 Matches
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NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
                                                                                                                                                                                1487 ТТТТААААААААААААААААААААААААААААА 1518
                                                                                                                                                                                                                                         1427 GTACTGTTTTTTTCTATCTTCTATATGTTTTAAAAGTATAATAATAAAAATATTTAATTTTT 1486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08545196B Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 205-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION UMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
                                                                                                                                                                                                   503 cttccaaaaaaaaaaaaaaaaaaaaaaaaaaa 534
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                               443 gttttgtaattttatattactttttagtttgatactaagtattaaacatatttctgtatt 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                         / Match 9.4%; Score 50.4; DB 3; Length 1582;
Local Similarity 71.7%; Pred. No. 0.0006;
nes 66; Conservative 0; Mismatches 26; Indels 0.
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CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22040-0747
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US-08-865-297-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 9.4%; Score 50.4; DB 3; Length 1582; Best Local Similarity 71.7%; Pred. No. 0.0006; Mismatches 66; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION: (703) 205-8000
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: The Siva Genes, No. 6010853el Genes Involved in TITLE OF INVENTION: CD27-Mediated Apoptosis
                                                                                                                                                                                                                                                                                                          APPLICANT: Prasad V.S. Kanteti, Zhaohui Ao, and Stuart F. APPLICANT: Schlossman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1487 ТТТТАЛААААААААААААААААААААААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1427 GTACTGTTTTTTTTCTATCTTCTATATGTTTAAAAGTATAATAATAAAAATATTTAATTTTT 1486
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 FILING DATE:
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               APPLICATION NUMBER:
                                                                                                                                                                                                 STREET: 60 St
CITY: Boston
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                                                                                                                                                                 COUNTRY:
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LENGTH: 1582 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/545,196B FILING DATE: 19-OCT-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: PO BOX 747
CITY: FALLS CHURCH
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                                                                                                                                                                               Massachusetts
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PO BOX 747
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UMBER: US/08/865,297
29-MAY-1997
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; NAME/KEY:
; LOCATION:
US-08-865-297-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 770 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
CLASSIFICATION: 435
ACTORNEY/AGENT INFORMATION:
ANAME: White, John P
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 cagaaaaagcctgtgcatgaaaaaaaagaagttttgtaatttttatattattatttttagttt 472
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628 CAGCACAAGATGTTCACACTAAAGAGAGAGAGAGGTGGCTTTTTATATGTTATGTTTTATA 687
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zeng, Li
TITLE OF INVENTION: AXIN GENE AND USES THEREOF
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748 AA 749
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                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                          CITY:
                                                                                                                        APPLICATION NUMBER: FILING DATE: 10-JUL
                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              n 8.8%;
Similarity 61.5%;
75; Conservative C
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                                                                                                                                                                                                                                                10036
                                                                                                                                                                                                                                                                                        New York
                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (617)227-7400
(617)227-5941
                                                                                                                                                                                                                                                                                                       E: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88..612
                                                                                                                                                                                                                                                                                                                                                                                                Constantini, Franklin
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                                                                                                                           10-JUL-1997
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                                                                                                                                           US/08/890,865A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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US-08-890-865A-2
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5194596-16
;Patent No. 5194596
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TITLE OF INVENTION: PRODUCTION OF VASCULAR ENDOTHELIAL CELL
                                                                                                                                                                                                                                                                                                                                                                                                     QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
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NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                       5219739-16
;Patent No. 5219739
;Patent No. 5219739
;APPLICANT: TISCHER, EDMUND G.;ABRAHAM, JUDITH A.;FIDDES,
APPLICATION NUMBER: 450,883
FILING DATE: 14-DEC-1989
APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
SEQ ID NO:16:
                                                                                                                                                   JOHN C.:MITCHELL, RICHARD L.

JOHN C.:MITCHELL, RICHARD L.

TITLE OF INVENTION: DNA SEQUENCES ENCODING BYEGF120 AND HUMAN
HVEGF 121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HVEGF121
VAASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BYEGF120 AND HVEGF121
NUMBER OF SEQUENCES: 40
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.4%; Score 45; DB 6; Length 961; Best Local Similarity 63.3%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3722 ТGAACCTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAA 3758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3662 AATGACTTGTACAATTATCTTTTCAAAGGTACTTGGATAATAATGAAATAAAAACGTTTT 3721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/
FILING DATE: 14-DEC-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 aagaagtittgtaattttatattacttittagtitgatactaagtattaaacatattict 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3761 base pairs TYPE: nucleic acid
                                                                                            APPLICATION NUMBER: US/
FILING DATE: 27-JUL-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 tgcatgaaaaaaaagaagttttgtaattttatattactttttagtttgatactaagtatt 485
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 387,545
FILING DATE: 27-JUL-1989
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                                                                                                                                         US/07/559,041
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 Mismatches

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LENGTH: 961

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US-09-448-076-1
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                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2920
                                                                                                                                                                                                                                                                  Sequence 1, Application US/09448076 Patent No. 6300092 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-276-400-1
                                                                                 CURRENT APPLICATION NUMBER: US/09/448,076 CURRENT FILING DATE: 1999-11-23 EARLIER APPLICATION NUMBER: 60/117,580 EARLIER FILING DATE: 1999-01-27 EARLIER APPLICATION NUMBER: 09/276,400 EARLIER APPLICATION NUMBER: 09/276,400 NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-276-400-1
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                                                                                                                                                                                                 APPLICANT: Khodadoust, Mehran et al.
TITLE OF INVENTION: METHODS OF USE OF A NOVEL LYSYL OXIDASE-RELATED PROTEIN
FILE REFERENCE: MNI-073CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-18 PROTEIN AND NUCLEIC ACID MOLECULES AND
FILE REFERENCE: MNI-073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09276400 Patent No. 6140056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/276,400 CURRENT FILING DATE: 1999-03-25 NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.3%; Pred. No. 0.012; Matches 69; Conservative 0; Mismatches 40; Indels
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (143)..(2401)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 8.4%; Score 44.6; DB 3; Length 2920; Local Similarity 68.1%; Pred. No. 0.023; les 62; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 tgcatgaaaaaaaagaagttttgtaattttatattacttttttagtttgatactaagtatt 485
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                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/946,026
FILING DATE: 07-OCT-1997
CLASSIFICATION: 424
ATTORNEE/JAGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.424
TELECOMMUNICATION INFORMATION:
TELEPHONE: (266) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-448-076-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/08946026 Patent No. 6034218
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                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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501 ttcttccaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 534
                                                   233 AACTTTGGAATATATGTTTGCCAATCTCCTTGTTTTCTAATGAATAAATGTTTTTATATA 292
                                                                                 441 aagttttgtaattttatattactttttagtttgatactaagtattaaacatatttctgta 500
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MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
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LOCATION: (14)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2880 cttcagaaaaaaaaaaaaaaaaaaaaa 2910
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Twardzik, Daniel R.

Mitcham, Jennifer L.

Mitcham, Jennifer L.

MITCHAM, JENNIFER AND METHODS FOR IMMUNOTHERAPY

NVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY

NVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
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RESULT 11
US-08-557-309B-22
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US-08-557-309B-22
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                                                                                                                                                                             Patent No.
                                                                                                                                                                                            Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/08/557,309B FILING DATE: 14-NOV-1995 CLASSIFICATION: 435
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Local Similarity 68.5%;
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                    ADDRESSEE:
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                                                                                                                                                                                            Application US/08834306
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Lodes, Michael J.
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6300 Columbia Center, 701 Fifth Avenue
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                  SEED and BERRY LLP
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 Mismatches

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                                                                           PREVENTION OF
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                    STATE:
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                                                                                                                                                                                                                                                                                        ADDRESSEE:
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Sequence 22, Appr. 8 --- No. 622837
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 581 base pairs
                                                                                                                                                                                                                                                                                                                          APPLICANT: Houghton, Raymond L.
APPLICANT: Smith, John M.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND NUMBER OF SEQUENCES: 81
                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                  FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                        CITY: Seattle
                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                       ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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Maki, David J.
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Lodes, Michael J.
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                                              UMBER: US/08/993,674A
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PREVENTION OF

REGISTRATION NUMBER:

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APPLICANT: Rothe, Mike
                                                                                                                                                                                                            TELEFAX: (415)398-324 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 base pairs
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                          TOPOLOGY:
                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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STRANDEDNESS: single
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Similarity 64.6%;
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                     Score 43; DB 4;
Pred. No. 0.057;
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                                   DB 4; Length 2589;
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                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415)398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTARNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-6:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
                                                               2468 AAAATAAGGATTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTG 2527
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                              436 aaaagaagttttgtaattttatattactttttagtttgatactaagtattaaacatattt 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
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FILING DATE: 06 AUG 1996
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.057;
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AC010289 Homo sapi

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435 aaaaagaagttttgtaattttatattacttttagtttgatactaagtattaaacatatt 494
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                                                431 AAAAAGAAGTTTTTTAATTTAATTTAGTTTTTAGTTTTGATACTAAGTATTAAACATATT
                                                                                                                375 tttaccggaagcttctgttcaatcccagcggtccttaccagaaaaagcctgtgcatgaaa 434
                                                                                                                                                   311 TTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTTGGCGACGGGGCCCTTA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
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/db_xref="GI:6288734"
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expression inhibited by IL-10"
/codon_start=1
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/db_xref="taxon:9606"
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Pred. No. 2.3e-116;
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495 tctgtattcttccaaaaaaaaaaaaaa 522
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                                                                                                                                                                  307 TTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCTTA
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Similarity 99.4%;
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
144 .443
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/codon_start=1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (07-SEP-2000) Immunology, Peking University Hea
Submitted (07-SEP-2000) Immunology, Peking University Hea
Science Center, Xueyuan Road 38, Beijing 100083, China
Science Center, Xueyuan Road 38, Beijing 100083, China
Science Center Submitter
Sequence update by submitter
Sequence version replaced gi:6630853.
Location/Qualifiers
                                                                                                       ctgggtctgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgct 194
                                                                                                                                                 ATCGCTTCGCAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTG 130
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TTTLTYGGGVFALVTAVCCLADGALIYRKLLFNPSGPYQKKPVHEKKEVL"
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/note="UCK-2; alternatively spliced"
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                                                                                                                                                                                                                                                                                      65.4%; Score 349.4; DB 9; Length 689; 76.4%; Pred. No. 4.8e-75;
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                                                                                                                                                                                                                                                                                                                        Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China 2 (bases 1 to 593)
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Han, W.L., Gu, W.F., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and
                                                                                                                                                                                                                                               Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China Sequence update by submitter
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                                                                                                                                                                                                                         2000 this sequence version replaced gi:6625671
Location/Qualifiers
                                                                                                                                                     /db_xref="taxon:9606"
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                                                                                   /gene="CKLF4"
                                                                                                                'note="UCK"
                                                                                                                           "CKLF4"
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                                                Direct Submission

Submitted (12-MAR-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                       Homo sapiens, clone MGC:10658
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Pred. No. 5 9e-75;
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Best Local Similarity Matches 507; Conserv
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289 gataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtgacagcagt 348
                                                     373 TGATATTATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTTGGCACT 432
                                                                                230 -gatattatcaactcactggtaacaacagtattcatgctcatcgtatctgtgttggcact 288
                                                                                                                                                   313 CATACTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTTGGCCTTTGCT 372
                                                                                                                                                                                                                                                   253 ACAAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTT 312
                                                                                                                                                                                                                                                                                                                                                   193 CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGC 252
                                                                                                                                                                                                                                                                                                                                                                                         208 ccacgtgaagatgctgcggctg----- 229
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9989692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Ree, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Pancreas, adenocarcinoma"
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/db_xref="taxon:9606"
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141 ctgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgcttcagtg 200
                                                                               21 ccgagctgggcgagaagtagggggggggggtgctccgccgcgggtggcggttgctatcgct 80
                                                                                                                            Local Similarity
                      655 bp mRNA linear PRI 31-DEC-:
Homo sapiens transmembrane proteolipid (C32) mRNA, complete Cds
AF057306
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic and Foundation, Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thang, J.S., Nelson, M., Wang, L. and Smith D.I.
                                                                                                                                                                                         171 a
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                               /note-"down regulated upon cell differentiation induced by sodium butyrate"
                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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137 c 153 g 194 t
                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pancreas"
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                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                            /gene="C32"
                                                                                                                                                                                                                                                                                                                                                                            /cell_line="AsPC-1"
                                                                                                                                                                                                                                                                     codon_start=1
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                                                                                                                                 60.9%;
75.6%;
                                                                                                                         0; Mismatches
                                                                                                                                 Score 325.4; DB 9; Length 655; pred. No. 3.5e-69;
                                                                                                                            1; Indels 159; Gaps
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AX061665
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                               polyA_site
                      ORIGIN
                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TCATCGCACAAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TGAAAGGCCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TATTTTCATACTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 -----gatattatcaactcactggtaacaacagtattcatgctcatcgtatctgtgt 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 gcggtccttaccagaaaaagcctgtgcatgaaaaaaaagaagttttgtaattttatatta 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                              source
                                                                                    sig_peptide
                                                          polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tggcactgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtga 341
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 70 from Patent W001100806.
AX061665
                                                                                                                                                                                                                                                                                                                                                                                  AX061665.1 GI:12406789
                                                                                                                                                                                                                                                                                                                                                                                                                      AX061665
                                                                                                                                                                                                                                                                  1 (bases 1 to 669) ... Bougueleret, L. and Jobert, S. dumas milne Edwards, J.B., Bougueleret, L. and Jobert, S. Complementary dna's encoding proteins with signal peptides patent: WO 0100806-A 70 04-JAN-2001;
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                       GENSET (FR)
                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                  /db_xref="G1:12406790"
/db_xref="G1:12406790"
/translation="munvopkikhrpeccesvkghvkmlrlalivtypmlivsvlalipe
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ryplivgggvfalvtavccladgaliyrkllfnpsgpyqkkpvhekkevt"
                                                  /note="Von Heijne matrix score 4.10 seq VFMLIVSVLALIP/ET" 630. .635 655. .669
                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                   /codon_start=1
                                                                                                                                                                            /note="unnamed protein product"
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                                           139 c
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Length 669;
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Query Match

Score 321.8; DB 6;

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REFERENCE
AUTHORS
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AF135381
                                                                                                                              REFERENCE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                        516 aaaaaaa 522
                                                                                                                                                                                                                                                                                                                                                                                                423 CTGTGTTGGCACTGATACCAGAAACCACAACATTGACAGTTGGTGGAGGGGGTGTTTGCAC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 ctgtgttggcactgataccagaaaccacaacattgacagttggtggaggggtgtttgcac 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 TTTGGCCTTTGCTTGATATTATCAACTCACTGGTAACAACAGTATTCATCCTCATCGTAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 TTATCTTATTTTTCATACTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGGTTAT 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 TCAGTGTGAAAGGCCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 ctgggtctgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgct 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ATCGCTTCGCAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGG--ATTGCTGCTG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 atcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctg 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 gtgaagccgagctgggcgagaagtaggggaggggggtgctccgccgcggtggcggttgct 74
  Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 GGGAAGCCGAGCTGGGCGAGAAGTAGGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCT 64
                                                     Direct Submission
Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 434)
Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.
                                                Han, W.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                      alternatively spliced.
                                                                                                                                                                                                                      AF135381 434 bp mRNA linear PRI 07-S
Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete
                                                                                                                                                                                                AF135381.2 GI:9989693
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Matches 423;
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                                                                                                                                                        375 tttaccggaagcttotgttcaatcccagcggtccttaccagaaaaagcctgtgcatgaaa 434
                                                                                                                                                                                                                                                                                275 TTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAAGCCTGTGCATGAAA 334
                                                                                                                                                                                                                                                                                                                                                   225 ------GGTGTTTTGCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCCTTA 274
                                                                                                                                                                                                                                                                                                                                                                      315 ttggtggagggtgtttgcacttgtgacagcagtatgctgtcttgccgacggggccctta 374
                                                                                                                                                                                                                                                                                                                                                                                                                                              255 cagtattcatgctcatcgtatctgtgttggcactgataccagaaaccacaacattgacag 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 TCAGTGTGAAAGGCCACGTGAAGATGCTGCGGCT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 ctgggtctgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgct 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 CTGGGTCTGCAGACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 ATCCCTTCCCAGAACCTACTCAGGCAGCCAGCTGAGAGAGTTGAGGGAAAGTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 gtgaagccgagctgggcgagaagtaggggagggggggtgctccgccgcggggtggcggttgct 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 81.38; tes 423; Conservative
G30204.1 GI:1593755
STS; STS sequence; primer; sequence tagged site.
                                                       human STS SHGC-36487, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctg 134
                                                                                           G30204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science Center, Xueyuan Road 38, Beijing 100083, China Sequence update by submitter On Sep 7, 2000 this sequence version replaced gi:6630855, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKLLFNPSGPYQKKPVHEKKEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAF19600.1"
/db_xref="G1:6630856"
/translation="MDNVQPKIKHRPFCFSVKGHVKMLRLVFALVTAVCCLADGALIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="chemokine-like factor 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="UCK-3; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CKLF3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_line="U937"
/note="from PHA stimulated cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                         linear
                                                                STS 05-0CT-1996
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                                                                                                                                                                                                                   Matches 281; Conservative
                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                              167 AGTATGCTGTCTTGCCGACGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGG
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                       actgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtgacagc 345
                                                                    agtatgctgtcttgccgacggggcccttatttaccggaagcttctgttcaatcccagcgg 405
                                                                                                           ACTGATACCAGAAACCACAACATTGACAGTTGGTGGAGGGGGTGTTTGCACTTGTGACAGC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 485)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myers, R.M.
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer A: ACTTCTTTTTTTTCATGCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                      prepared with primer pairs provided by Sandoz, derived from T90569
-- Washington University/Merck EST sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Profile:
                                                                                                                                                                                                                                                                                                   146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermal Cycler:
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PCR Cycles:
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Taq Polymerase:
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69. .91
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a 99 c 99 g
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                                                                                                                                                                                                                                                                                                                                                  /map="16"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                 52.1%;
97.9%;
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                 Score 278; DB 11; Length 485; Pred. No. 1.3e-57;
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50 mM
20 mM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 97083)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 97083)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center
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                                                                                                                                                                                                                                                                                                                                                                     pirect Submission
Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Sep 6, 2001 this sequence version replaced gi:15147148.
Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-15863 G24307
                                                                                                                                                                                                                                                                                                                                                      www.jgi.doe.gov
                                                                                                                                                                                                                                                   STS Content:
                                                                                                                                                                                                                                                                                        Quality: Phrap Quality >=40 99.8% of Sequence;
                                                                                                                                                                                                                                                                                                            www-shgc.stanford.edu
                                                                                                                                              position 96045
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                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                      Location/Qualifiers
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Query Match 40.1%; Best Local Similarity 99.5%;

Matches 215;

Conservative

0; Mismatches Score 214.4; DB 9 Pred. No. 1.2e-41;

DB 9;

Length 97083; Indels

0; Gaps

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sum-of-contigs agarose-fp

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 30, 2000 this sequence version replaced gi:6692324. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 151620)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Assembly program: Phrap; version 0.960731 consensus quality: 141737 bases at least 040 consensus quality: 145736 bases at least 030 consensus quality: 145736 bases at least 020
                                                                                                            Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                      Center clone name: 13_P_4
                                                                                                                                                                                                                               Center project Information
                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 151620)
                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
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Insert size: 149920; sum-of-contigs
Quality coverage: 4.6 in Q20 bases;
Quality coverage: 5.5 in Q20 bases;
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* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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89511 113391: contig of 23881 bp in length
113392 113491: gap of 100 bp
113492 151620: contig of 38129 bp in length.
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2327 2426: gap of 10
2427 4519: contig of
4520 4619: gap of 10
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/note="assembly_fragment"
22583. .26540
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62475: contig of 9401 bp in length
62575: gap of 100 bp
72661: contig of 10086 bp in length
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62475: con
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52974: contig of 10620 bp in length
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30917: contig of 4277 bp in length
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Homo sapiens chromosome 16 clone RP11-403P17, complete sequence.
AC010542
Direct Submission Submitted (31-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 31, 2001 this sequence version replaced gi:13786333. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 188460)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                          Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 188460) DOE Joint Genome Institute and Stanford Human Genome Center.
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26641. .30917
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89511. .113391
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Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.5.
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Finishing Completed at Stanford Human Genome Center
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                                                                                                                                                                                                                Cancer gene determination and therapeutic screening using signature
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Patent: W
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Cancer gene determination and therapeutic screening using signature
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                Score 205; DB 6; Length 207; Pred. No. 7.3e-40;
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                                                                  PAT 09-JAN-2002
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                   Query Match 38.4%; Score 205; DB 6; Length 207; Best Local Similarity 99.5%; Pred. No. 7.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                    483 attaaacatatttctgtattcttcca 508
                                                                147 ACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGNAAAAGC 88
                                                                                                                                                        363 acggggcccttatttaccggaagcttctgttcaatcccagcggtccttaccagaaaaagc 422
                                                                                                                                                                                                         207 CAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTTGCCG 148
                                                                                                                                                                                                                              303 caacattgacagttggtggaggggtgtttgcacttgtgacagcagtatgctgtcttgccg 362
27 ATTAAACATATTTCTGTATTCTTCCA 2
                                                                                                                                                                                                                                                                                           205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avalon Pharmaceuticals (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent:
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                                                                                                                                                                                                                                                                                                                                                                                                    70 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO 0194629-A 1517 13-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
a 43 c 39 g 5/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                         0; Mismatches
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Search completed: July 17, 2002, 09:19:58 Job time: 11688 sec

6.8e+03

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OM of: US-09-801-115-2 to: Issued_Patents_NA:* out_format:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Jul 17, 2002 11:34 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patabase sequences: 383533
patabase length: 122816752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-377-155-14 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-801-115-2
          _6/ptodata/2/ina/6B_COMB.seq:US-09-669-974-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Issued_Patents_NA: *
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59.50
59.50
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            120.13
             96.95
96.95
18 28.05
18 28.05
08 28.05
08 277
5 52.77
13 52.90
                                                                                                                  314.24
1 630.46
1 630.46
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1435
3706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                   US-09-385-982-95
                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 95
LENGTH: 392
                                            seq_documentation_block:
                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                          Sequence 11, Application US/09251645 Patent No. 6281413
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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No. 6262334
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Ratio:
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-385-982-95
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CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER FILING DATE: 1998-08-31
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-251-645-11
                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-385-982-95 from: 1 to: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us-09-801-115-2 \times us-09-385-982-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: (1)...(392) OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                        144 TGTTTGCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCTTATT 193
                                                                                                                         42 rValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyGlyV 59
                                            244 GCATGAAAAAAA 256
                                                                                                                                                                                                                                             59 alpheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIle 75
                                                                                                                                                                                                                                                                                       94 TGTGTTGGCACTGATACCAGAAACCACAACATTGACAGTTGGTGGAGGGG 143
                                                                                 92 lHisGluLysLys 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09385982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357.00
5.028
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seq_documentation_block:
   Sequence 11, Application US/09116498
   Patent No. 6251582
                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-116-498-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
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NAME/KEY: CDS
LOCATION: (31393)..(35838)
OTHER INFORMATION: orf2
US-09-251-645-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-801-115-2 x US-09-251-645-11
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GENERAL INFORMATION:
                                                                                                                                        6690 ATCAG 6694
                                                                                                                                                                                               6662 .....ATATTTCAGCCATCAAACTGGAGTCCTC 6689
                                                                                                                                                                                                                                                                           6620 ATGATTGGGGAGATGGCTATC.....TGAGTATGGTGTATGGCGGAA.. 6661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 11
LENGTH: 37948
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                          6570 CTATGCAGAAAGCTACGAAATCCCTTCATCAGTAAATAGTAATAACGGTT 6619
                                                                                                                                                                                                                                                                                                                                                                                                                                    6526 TATAAACAGTTTGATA......CTAATAGTATTATTGGTGTGAATAATCG 6569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6476 CCAATATGTCTTCTAAGGAAATGACACCTGAAAATCACAAACCTAACGCT 6525
                                                                                                                                                                            87 yrGln 88
                                                                                                                                                                                                                                   72 yAlaLeuIleTyrArgLysLeuLeuPheAsnProSer......GlyProT 87
                                                                                                                                                                                                                                                                                                                  56 GlyGlyGlyValPheAlaLeuValThrAlaValCysCysLeuAlaAspGl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (23768)..(31336)
OTHER INFORMATION: hph2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Anderson, Arne R.
APPLICANT: Hart, Hope
                                                                                                                                                                                                                                                                                                                                                                                              45 laLeuIleProGluThrThrThrLeu.....ThrVal 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (15171)..(18035)
OTHER INFORMATION: Orf5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dunn, Martha APPLICANT: Chen, Jeng S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 eIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAspIl 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Warren, Gregory W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
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alignment_block:
US-09-801-115-2 x US-09-116-498-11
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-116-498-11 from: 1 to: 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 48.315
628 .....AGCATTGTGACCTGCTACTGTTGCATTGCA...... 657
                                                                                                                                                    617 TCCCTTTGTTG ......
                                                                                                                                                                                                                                                                                             567 TCCACTTAAACTCATATGGTCCCTGGTGGCCTTAATTTTCACCTTTTTTG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 base pairs
                                                                    58 GlyValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLe 74
                                                                                                                                                                                                                    41 alSerValLeuAlaLeuTleProGluThrThrThrLeuThrValGlyGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                         529 ATTGATGATAAGCCATACTGT......GCAGAGAAAAAGGCAAC 566
                                                                                                                                                                                                                                                                                                                                                                     24 uArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIleV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 IleLysHisArgProPheCysPheSerValLysGlyHisValLysMetLe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: pigtail macaque SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unutmaz, Derya
Ramani, Vineet N.K.
Ramani, Vin
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Deng, Hongkui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/116,498 FILING DATE: 16-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Ave,
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1.698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Esq.
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-116-498-7

689 GAAAGCACAACAAAAAG 705

91 rovalHisGluLysLys 96

658AGGAAGCTGTGTGCCCAT.....TACCAGCAGTCAG 688

74 ulleTyrArgLysLeuLeuPheAsnProSerGlyProTyrGlnLysLysP 91

seq_documentation_block:

Sequence 7, Application US/09116498 Patent No. 6251582 GENERAL INFORMATION:

APPLICANT: Littman, Dan R.

Deng, Hongkui

CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson,

EE: David A. Jackson, Esq. 411 Hackensack Ave, Continental Plaza, 4th

CITY: Hackensack

LTOOL

New Jersey

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COUNTRY: USA

NUMBER OF SEQUENCES:

```
Unutimaz, Derya
Ramani, Vineet N.K.
Ramani, Vineet N.K.
NOVEL ALTERNATIVE G-COUPLED RECEPTORS
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
ASSOCIATED WITH SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
    Sequence 2, Application US/08061092A
    Patent No. 5587458

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-061-092A-2
                                                                                                                            NAME/KEY:
;
LOCATION:
US-08-061-092A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: KING,
                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 ATTGATGATAAGCCATACTGT......GCAGAGAAAAAGGCAAC 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 TCCAATTAAACTCATATGGTCCCTGGTGGCCTTAATTTTCACCTTTTTTG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 TCCCTTTGTTG......627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 ......AGGAAGCTGTGTGCCCAT......TACCAGCAATCAG 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 alSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 689 GAAAGCACAACAAAAAG 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 uArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIleV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GlyValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 ulleTyrArgLysLeuLeuPheAsnProSerGlyProTyrGlnLysLysP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTI-erbB-2 ANTIBODIES, COMBINATIONS
THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 roValHisGluLysLys 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER READABLE FORM:

OPERATING SYSTEM: PC COMPATIBLE
COMPATIBLE
COMPUTER READABLE FORM:

OPERATING SYSTEM: PC COMPATIBLE
COMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
       Quality:
                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        George Mason Bldg., Washington & Prince Sts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KING, C R
KASPRZYK, Philip G
                                                                                                                                                                                                                                                                                                                                                                                                               720 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burns, Doane, Swecker & Mathis
                                                                                                                                                                            1..720
                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                            double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        018797-014
                  Length:
Gaps:
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alignment_block: alignment_scores: Align seg 1/1 to: US-09-116-498-7 from: 1 to: 1083 US-09-801-115-2 x US-09-116-498-7 Percent Similarity: 8 IleLysHisArgProPheCysPheSerValLysGlyHisValLysMetLe 24 Quality: Ratio: ::: | | | ::: | | 48.315 71.00 1.651 Gaps: 4
Percent Identity: 26.966

US-09-116-498-7

ORGANISM: Homo sapiens SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ORIGINAL SOURCE: HYPOTHETICAL:

RAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 1049-1-009
REFERENCE/DOCKET NUMBER: 101-009
TELEPAX: 201-487-5800
TELEPAX: 1083 base pairs
LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Unl-1998
CLASSIFICATION: <UDKnown>
ATTORNEY/AGENT INFORMATION:

CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

Ratio:

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CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 43676
TYPE: DNA
                                                                                                                                                                                                                                                                                            alignment_block;
                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                      Align seg 1/1 to reverse of: US-09-356-952-12 from: 1 to: 43676
                                                                                                                                                                                                                                                         US-09-801-115-2 x US-09-356-952-12/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                       / ORGANISM: Saccharomyces cerevisiae US-09-356-952-12
                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                         43548 TACACAATATATGAAAGTTAATGTGGATTTGTCCAAATTCGTCGATGGGC 43499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-356-952-12
                                                                                                                        43598 GTCCGTAAGGCTTTGCTTTGTATCGTTAGTGCATTCTCACTTATTTCAAA 43549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Borr-Sogi, Dafna
APPLICANT: Borr-Sogi, Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
FILE REFERENCE: 600-1-228N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09356952
Patent No. 6117663
59 alPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIle 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: US-08-061-092A-2 from: 1 to: 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-801-115-2 x US-08-061-092A-2/rev
                                                                            49 uThrThrTheuThrValGly......GlyGlyV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 58.333 Percent Identity: 30.556
                                                                                                                                                               33 ValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGl 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       502 ATCCAATCCATTCCAG 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 GCCCTGGAATTTCGGGTCATATACAGTATTACCATTCTCAGGATGAATCC 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584 TTGGAGGA......TGTGTCTGCTGTTATACTGGCCTT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               634 AGACGGCAGTGTCCTCAGATGTCAGGCTGCTGAGGTGAAGGTAGGCCGCG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 oSerGlyProTyrGln 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              684 GTAGTACATAGCATAGTAAGCACTATAGTAGTAATAAGAAGCACAGTAAT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AlaLeuIleTyrArgLys.....LeuLeuPheAsnPr 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 ..GlyGlyValPheAlaLeuValThrAlaValCysCysLeuAlaAspGly 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 u......AlaLeuIleProGluThrThrThrLeuThrValGly.... 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLe 44
                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                         65.50 Length: 78
1.523 Gaps: 3
55.128 Percent Identity: 33.333
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alignment_block:
US-09-801-115-2 x US-08-684-862-9/rev
                                                                                                                                                alignment_scores:
Align seg 1/1 to reverse of: US-08-684-862-9 from: 1 to: 1333
                                                                                                                                                                                                    US-08-684-862-9
                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-684-862-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08684862 Patent No. 5759541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Bach, Alfred
APPLICANT: Hillen, Heinz
APPLICANT: Bialojan, Siegfried
TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43398 ATCAGTTAACGTTTCTACCAAAGCAGAACTTCTG 43365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM.

MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: ISM AT-compatible, 80286 processor OPERATING SYSTEM: MS-DOS version 5.0
                                                                                                                                                                                           TOCATION: 231 to 935
OTHER INFORMATION: the coding region shown in (2)(ix)(B)
OTHER INFORMATION: codes for the protein of SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect version 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43448 TATAGATCGCTAAGGTTGGCTGACCCACTCAATAACGAAATAATAAAACC 43399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ### 43498 TTTACGCGCTATTACCTTATATCTGTCTTGATGCAGACATCGAATTATCT 43449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/966,040 FILING DATE: 30-DEC-1992 APPLICATION NUMBER: PCT/EP91/01 FILING DATE: 19-JUL-1991
                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/361,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1101 Conn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 o......ValHisGluLysLysGluValLeu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 TyrArgLysLeu...LeuDheAsnProSerGlyProTyrGlnLysLysPr 91
                                                                                                                              Quality:
                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                         Agkistrodon rhodostoma
                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                           cDNA to mRNA
                                                                                2.150 Gaps: 2
53.571 Percent Identity: 33.929
                                                                                                                              64.50
                                                                                                                                                                                                                                                                                                                                             single
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                                                                                                                       Length:
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-462-844-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Bacillus subtilis US-09-462-844-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 1, Application US/09462844 patent No. 6258563
                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-801-115-2 x US-09-462-844-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: Increasing production of Proteins in
TITLE OF INVENTION: Gram-positive Microorganisms
FILE REFERENCE: GC385-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1196 ......AAGTTGTTTTTTCCAATTCTTGTGATTTC... 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1245 TATCCAATCTGTTTTCTTGTCCTCAGATTTAGTTTGCTGTCTAAGGGAT. 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: EP 97305286.3
PRIOR FILING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: 1997-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OURRENT APPLICATION NUMBER: US/09/462,844
CURRENT FILING DATE: 2000-01-13
CURRENT FILING DATE: PCT/US98/14786
PRIOR APPLICATION NUMBER: PCT/US98/14786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1166 .....cccccccacaag 1155
                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-462-844-1 from: 1 to: 2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: EP 97305344.0 PRIOR FILING DATE: 1997-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 LeuileValSerValLeuAlaLeuIleProGluThrThrThrLeuThrVa 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 lyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyrGln 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 1GlyGlyCalPheAlaLeuValThrAlaValCysCysLeuAlaAspG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 LysLysProValHisGlu 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 2211
                                                                                                                                                                                                                                                                                        1132 TCTGTTAAAGGGTTTGCGACAATGCTGATCCTATCGATTTTGACAAGCTT 1181
                                                                                                                                                                                                                  1182 TATCACTGCCGTTTTC...TTATCGAGATTTCTCCTCGCTCTCCTTGTGG 1228
                                                                                                                                             1290 TATTCAGGATACGGATGAAAATACAGAGCCGCATACGCCATTCCAAAAAT 1339
                                                                                                                                                                                                                                                                                                                        16 ServallysGlyHisVallysMetLeuArgLeuAspIleIleAsnSerLe 32
                                                                                                                                                                                                                                                    32 uValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProG 49
                                                                                                                                                                             49 luThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAla 65
                                                                                                       66 ValCysCysLeuAlaAspGlyAlaLeuTleTyrArgLysLeuLeuPheAs 82
                                 82 n.....proSerGlyProTyrGlnLysL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.50 Gaps: 3
1.402 Gaps: 28.571
50.549 Percent Identity: 28.571
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-772-270A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08772270A patent No. 6019984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1340 GGGATTTCACGAGCAAACGCAAA 1362
                                                                                                                                                                                                                                                                                                                                       US-08-772-270A-14
                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MacInnes, Janet
APPLICANT: Ricciatti, Paul
APPLICANT: Mallard, Bonnie
                                                                                                                                                                       Align seg 1/1 to reverse of: US-08-772-270A-14 from: 1 to: 7721
                                                                                                                                                                                                     us-09-801-115-2 \times us-08-772-270A-14/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 ysProValHisGluLysLysGlu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto
                                                                                                                  ::: |||||||||:::::|||
7519 CGTTCTCTTAGACTTTCAGTAATAGATTCTTCTAATGGACTGAGTAGGAA 7470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                        7469 ACTGATAACACTGCGTTCTCCTGTTTTAATTTCTGCAATAACGCTCATTC 7420
7419 CAGAACCTAATTGAATTTCTTTATCACCATCTGTTAATGTTTTCTTGTTA 7370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 65
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                     32 .LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleP 48
                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                           48 rogluThrThr......ThrLeuThrValGlyGlyValpheAlaLeu 62
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                                                                                                                                                                                                                                                                       Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                       1.240
51.485
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                                                                                                                                                                                                                                                           percent Identity: 22.772
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alignment_block:
US-09-801-115-2 x US-08-976-259-70
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Quality:
Align seg 1/1 to: US-08-976-259-70 from: 1 to: 17710
                                                                                                   Quality: 64.00
Ratio: 1.231
Percent Similarity: 52.000
                                                                                                                                                                                                                     TOPOLOGY: 08-976-259-70
                                                                                                                                                                                                                                     NAME: STEFFE, ETIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
TYPOTTETATTON: 536
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Sequence 70, Applicati
Patent No. 6316609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Dillon, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-976-259-70
                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/ACENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7319 ATCAAGAGTAATAGTTTTTACTTTTCCATAGAGATAACCATATCTTGTGT 7270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7369 ATCTCAATAATAGAATTGAAAACTAAACCAAGCTGAGGGTGCTCAATAGC 7320
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                                                                                                                                                                                                                                   linear
                                                                                       Percent Identity: 25.000
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YPE:	: lin	TYPE: nucleic acid	RISTICS:	ORMATION FOR SEQ	-541-8587	ATION INFORMATT	TRATION NUME	NAME: Meigs, T Timeth:	ATTORNEY ACTION 31-DEC-1996	2001	PRIOR ADDITION: 435	FILING DATE: 24-DEC-1997		ARE: PatentIn Release #1 0	,=	TYPE: Floppy	COMPUTER READABLE FORM.	COUNTRY: USA	מסי	STREET: 3054 Cornwallis Road	392642744	SEQUENCES: 1152	AND USES THEBE	Rebischung, Corinne		APPLICANT: Steiner, Sabine	ANT: Philippe	6239264	tation_block: 176, Application US/ORGOR/16	 seq_name: /cgn2 6/htp3-11/2000	GTCAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	73 laLeuIleTvrArgIvsI	GCAGTTCATCA	58 VValPheals	17316 ACAACCGGCCCTGGCATATATATATATATATATATATATA	42 SerValLeuAlarenTlebroch.T	17266 ACAAAGTGAAGGGGTCGCTTGGTCACACACACACACACAC	25 rgLeuAspIleIleAspSerLeuValThrThrThrThrThrThrThrThrThrThrThrThrThrT	TTCAGAAGGGACCGGTGCAGGAAATATACACTACTACTACTACTACTACTACTACTACTAC	18	17166 GTTCAGGGTATGCTGAAGCATATTGATTTTTTCAGCGGGGGGTATGCTGAAGCATATTGATTTTTTTT	4 ValGlnProLysIleLysHisArgproBhog

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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1785
TYPE: DNA
ORGANISM: Neisseria meningitidis
FEATURE:
FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
US-09-377-155-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                               FILE REFERENCE: 065064/0128

CURRENT APPLICATION NUMBER: US/09/377,155

CURRENT FILING DATE: 1999-08-19

PRIOR APPLICATION NUMBER: CT/AU98/01031

PRIOR FILING DATE: 1998-12-14

PRIOR APPLICATION NUMBER: GB 9726398.2
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 CACAGCTATATATTGGCCCGCCGTCTCGCGCGCGCTGCTTGGGGAGCCGACT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427 GACCCCACCCTGATAGTGCCGTTGCAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 CGCCGTATAGCCTTGCTATATATACTTACGCTGCGACGCCCTATTCCGGA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 CTTCTCTCCGCCATAAGTGCGGAGCTGTTATCTATGCTACTCAAGCTCC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TGCTGCTGTGGGTATGCCGCAGACCGCGCCCTCACCAGCGGCGGCCAGC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 CTCGTGCTTGCCATCGTAGTTCCAGTCTACGGACTGCGCCTCCTGGTCTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 TTGGGGCCTTTCAACTCGTCCAGCGTGGACGCCTCTGATGCCTGTGCGAA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ...GlyValPheAlaLeuValThr.....AlaValCysCysLeuAlaAsp 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 ......ArgLysLeuLeuPheAsnProSer 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 uAlaLeuIle.....ProGluThrThrThrLeuThrValGlyGly.... 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLe 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyProTyrGlnLysLysProValHis 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....GlyAlaLeuIleTyr.....
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Ratio:
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1.351
43.119
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UMBER: GB 9726398.2
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alignment_scores:

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alignment_block: us-09-801-115-2 \times us-09-669-974-8/rev
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; LOCATION: (1)..(1782)
US-09-669-974-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul: APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PGT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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                                                                                                          Align seg 1/1 to reverse of: US-09-669-974-8 from: 1 to: 1785
                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-09-377-155-8 from: 1 to: 1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        826 TTTTAACTTCGGTTCTCTTGCCGTTGTCTTTGCTTTCCACATTAACAGTC 777
926 AAGCCTTCGCCTTTGTCTGTAGAAGAATCATTCTCGCCTTTGTCTTTACC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              876 AGTAACCAACTTACCGTCTTTTTTTTTTGATAACAGAAGTCTTCGCACCGA 827
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                                            11 ArgProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAs 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GlyGlyGlyValPheAlaLeuVal.ThrAlaValCysCysLeuAlaAspG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 euIleValSerValLeuAlaLeuIleProGluThrThrThrLeuThrVal 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 pIleIleAsn..... SerLeuValThrThrValPheMet...L 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ArgProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAs 27
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Ratio:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-367-206-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-801-115-2 x US-09-367-206-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 6
LENGTH: 2153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/367,206
CURRENT FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: PCT/US99/08847
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 60/082,767
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 60/113,296
PRIOR FILING DATE: 1998-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NSP Molecules FILE REFERENCE: P1223R1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                         1602 ACTATGGGCAACATGTTCAGCTTCGCGGCGGTCATGGGTGCCCTGGACAT 1651
                                                                                                                                                                                                                                                                                                                                                                                                                1502 CATCATGCTGGCCGTGGACATCCTGGGCTGCACCGGCTCTGCGGAGGAGC 155:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1452 CATGGCCGGCAGCTACGCCTAGACCTGCTGGAAAGGTTCCACACCATGTC 1501
                                                         1652 GGCTCAGATTTCTCGGCTGGAGCAGACATGGGTGACCCTGCGGCAGCGAC 1701
                                                                                                                                                                                                                                                                                                1552 GGGCAGCGCTGCTGCACAAGACCATTCAGCTGGCGGCCGAGCTACGGGGG 160:
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70 ..AlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 lPheMetLeuIleValSerValLeu...... 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HisValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrVa 36
                                                                                                                                                                                                                                                                                                                                                   .....AlaLeuIleProGluThrThrThrLeuThrValGly...... 56
                                                                                                                                                                                                                                   ......GlyGlyValPheAlaLeuValThrAlaValCysCysLeu..... 69
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Percent Identity: 24.107
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-249-420-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908) 594-472
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1702 ACACAGAGGGTGCCATCCTGTACGAGAAGAAGCTC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Carty, Christine E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Carty, Christine E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: El-Sherbeini, Mohamed APPLICANT: Clemas, Joseph TITLE OF INVENTION: DNA ENCODING GLS1
594 TCGTCTAGAAGCCATGAATTCACTCGTTACT
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1854 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Christine E. Carty
                                                                                    544 ATTATCCACAAGCAATTTTGTACAAAGTGAAAAGGTTGAACTAATTATCT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                            24 uArgLeuAspIleIleAsnSerLeuValThr 34
                                                                                                                        8 IleLysHisArgProPheCysPheSerValLysGlyHisValLysMetLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 07065-0900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rahway
STATE: New J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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Percent Identity: 51.852
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Title:
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AIC78580
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AV754613
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  BG613984
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BG249994
BF399486
BG529072
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 BG705303 602687808
BG24994 60236262
BF39948 017-R-CA1-
BG529072 602579169
BM472086 AGENCOURT
BG031757 602299819
BF691818 602247787
BF109912 7171f03.x
BF203359 601865968
A1078880 0237h05.x
A1742335 wg90a02.x
AV754613 AV754613
AA429945 zw67f10.s
AN455042 aa04a07.s
AX12804 qa94b08.s
AX125084 A02641513
AV759888 AV759888
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57.3		59.7												67.0	67.7	68.0	70.1	71.3	72.0	72.3	73.2	73.9	74.7	74.8	75.4	75.5	77.2	
ω ω	491	319	678	325	326	331	381	789	333	380	409	692	353	456	389	522	468	395	386	386	391	396	399	402	409	815	543	
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ALIGNMENTS

FEATURES SOUTCE		REFERENCE AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BG705303 LOCUS DEFINITION
	Email: cgapbs remail.nin.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA, Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	l (bases 1 to 524) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	BG705303.1 GI:13979504 BG705303.1 GI:13979504 EST. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	BG705303 524 bp mRNA linear EST 07-MAY-2001. 602687808F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820568 5', mRNA sequence.

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KEYWORDS
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                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                  Contact: Robert Strausberg, Ph.D
                                                                                                                      Unpublished (1999)
                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                        602362062F1 NIH_MGC_90 Homo sapiens cDNA clone
CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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   Rattus norvegicus
Eukaryota; Metazoa; Chordata;
                                                                                        510 bp mRNA linear EU-R-CA1-bjb-b-12-0-UI.sl UI-R-CA1 Rattus norvegicus UI-R-CA1-bjb-b-12-0-UI 3', mRNA sequence.
                                Norway rat.
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                                                              BF399486
BF399486.1
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/note="organ: liver; Vector: pCwV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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99.6%;
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Pred. No. 2.5e-60;
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The sequence contained an oligo-dT track that was present in the
Oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail.cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovery
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/lab_host-"DH10B (Life Technologies) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/library is a subtracted illamus, medulla, pons
/nidbrain, cerebral cortex, corpus striatum, testis, and
/nidbrain, cerebral cortex, corpus striatum,
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/db_xref="taxon:10116"
/clone="UI-R-CAI-bjb-b-12-0-UI"
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131 c 104 g
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National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 475.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                            228 a
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                /tisue_type="adenocarcinoma"
/lab_host="bH10B (T1 phage-resistant)"
/lab_host="bH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (Glontech);
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
/note="Organ: prostate; Vector: pDNR-LIB (Glontech);
/note="Organ: pDNR-LIB (Clontech);
/note="Or
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157 c
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/clone="IMAGE:4713305"
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98.7%;
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                                                                                                                                                                                                                                                                   High quality sequence stop: 486.
                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12328 row: a column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
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                 135
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/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sal; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 103 c 121 g 128 t
                                                                                                                                                    /Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5576339"
/clone_lib="NIH_MGC_92"
                                                                                                                                                                                                                                                      location/Qualifiers
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481 AAAAAAA 487
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                                          TTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCA
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                                                                                                        CTGTGTTGGCACTGATACCAGAAACCACAACATTGACAGTTGGTGGAGGGGGTGTTTGCAC
                                                                                                                                                                                                           ctgtgttggcactgataccagaaaccacaacattgacagttggtggaggggtgtttgcac
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REFERENCE AUTHORS FEATURES COMMENT SOURCE KEYWORDS VERSION ACCESSION DEFINITION BG031757 JOURNAL TITLE ORGANISM source found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10089 row: e column: 06 High quality sequence stop: 446. Email: cgapbs-r@mail.nih.gov Tissue Procurement: DCTD/DTP Unpublished (1999)
Contact: Robert Strausberg, Ph.D. NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 534) Homo sapiens 602299819F1 NIH_MGC_87 Homo sapiens BG031757.1 GI:12422364 mRNA sequence. BG031757 BG031757 DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium Location/Qualifiers 534 bp mRNA cDNA clone IMAGE:4394093 5', linear EST 24-JAN-2001

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BASE COUNT
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                                    AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCGCAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGTGAAGATGCTGCGGCTGGATATTATCAACTCACTGGTAACAACAGTATTCATGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                     caaaaaaaaaaaaaaaaaaaaaa 534
                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 529)
                                                                                                                                                                                          BF691818.1 GI:11977226
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                                                                                                                                                                                                                                                602247787F1 NIH_MGC_62 Homo sapiens
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Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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/clone="IMAGE:4394093"
/clone_lib="NIH_MGC_87"
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    tcttccaaaaaaa 514
                                      AAGTTTGTAATTTATATTACTTTTAGTTTGATACTAAGTATTAAACATATTTCTGTAT
                                                               agttttgtaattttatattactttttagtttgatactaagtattaaacatatttctgtat
                                                                                                                         AAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAAGCCTGTGCATGAAACAAAACAG
                                                                                                                                            aagettetgtteaateeeageggteettaeeagaaaaageetgtgeatgaaaaaaaga-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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/lab_host="DH10B (TI phage resistant)"
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: skin; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCAGGCGGCGACATG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
39 a 119 c 138 g 133 t
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286 actgataccagaaaccacaacattgacagttggtggaggggtgtttgcacttgtgacagc
                                                                                                                                                                                                 166 gccgaaaataaaacatcgccccttctgcttcagtgtgaaaggccacgtgaagatgctgcg 225
                                                                                                                                                                                                                                                                                408
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                                                                            GCTGGATATTATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGC
                                                                                                        gctggatattatcaactcactggtaacaacagtattcatgctcatcgtatctgtgttggc
                                                                                                                                                                                                                                                                      CTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGATGGATAACGTGCA 349
                                                                                                                                                                                                                                                                                               ctgagaagagttgagggaaagtgctgctgctgggtctgcagacgcgatggataacgtgca 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF109912 468 bp mRNA linear EST 20-OCT-2000 7171f03.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3526805 3' similar to TR:Q9UI41 Q9UI41 CHEMOKINE-LIKE FACTOR
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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61 AGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGC
                85 agaacctactcaggcagccagctgagaagagttgagggaaagtgctgctgctggtgtctgc 144
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                                                                      GCTGGGCAACAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCGC
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                                                                                                                                             503;
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTG-TTGCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCCTTATTTACCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCACAACATTGACAGTTGGTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gctcatcgtatctgtgttggcactgataccagaaaccacaaacattgacagttggtggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggccacgtgaagatgctgcggctggatattatcaactcactggtaaccaacagtattcat 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggtgttttgcacttgtgacagcagtatgctgtcttgccgacggggcccttatttaccggaa 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGCCACGTGAAGATGCTGCGGCTGGATATTATCAACTCACTGGTAACAACAGTATTCAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCACAAAAAAAAAAAAAAAAAAAAAAAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tccaaaaaaaaaaaaaaaaaaaaaaa 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITGAATTTATATTACTTTTAG-TTGATACTAAGTATTAAACATATTTCTGTATTCT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A10/8580 452 bp mRNA linear oz37h05.xl Soares_NhHMPu_S1 Homo sapiens cDNA clone 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
    125
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-499479."
                                                                                                                                                                                                                                                    pregnant uterus"
                                                                                                                                                                                                                                                                                           /clone="IMAGE:1677561"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                       /tissue_type="Pooled human melanocyte,
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                  host="DH10B"
                                                                                                                                                                                                                                                                               fetal heart,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
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                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 AACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTTGGCACTGATACCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aactcactggtaacaacagtattcatgctcatcgtatctgtgtttggcactgataccagaa 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aagcctgtgcatgaaaaaaaagaagttttgtaattttatattactttttagtttgatact 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTGAAGATGCTGCGGCTGGATATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
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                                                                                                                                                                                                       COntact: Nover 2017 (Contact Nover 2017) (Contact Nover 2017) (Contact the Email: clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. The Third Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE:2372330 3', mRNA sequence.
AI743235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI743235 453 bp mRNA linear EST 20-DEC wg90a02.xl Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
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                                                                                                                                                                                                     primer:
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      /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized
                                                                                                    /clone="IMAGE: 2372330"
                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                   r: -40UP from Gibco.
Location/Qualifiers
                                                                   /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
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Pred. No. 1.7e-54;
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AV754613
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448;
                                      Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R., Ye,M., Zhang,O., Han,Z., Chen,Z. and Chen,J.
Homo sapiens TP library cDNA clones
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 533)
                                                                                                                                                                                                                                                                                                 AV/54613 TP Homo sapiens cDNA clone TPAAOA11 5', mRNA sequence.
                    Unpublished (2000)
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                    AV754613.1
                                                                                                                                                                                                                                         human.
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Qinghua
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Zhang
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Pred. No. 1.6e-53;
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COMMENT

SOURCE KEYWORDS VERSION ACCESSION

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sapiens

cDNA clone

IMAGE: 781291

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                                                                                                                 504 TTTCTGTATTCTTACAAAAAAAAAAAAAAA 533
                                                                                                                                     493 tttctgtattcttccaaaaaaaaaaaaaaa 522
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                                                                                                                                                                                  AAAAAAAGAAG----GTAATTTTATATTACTTTTAGTTTGATACTAAGTATTAAACATA
                                                                                                                                                                                                  aaaaaaagaagttttgtaattttattatttactttttagttttgatactaagtattaaacata 492
                                                                                                                                                                                                                                                   TATTTACCGGAAGCTTCTGTTCAATCCCANCGGTCCTTACCAGAAAAAGCCTGNGCATGA
                                                                                                                                                                                                                                                                                                                                     agttggtggaggggtgtttgcacttgtgacagcagtatgctgtcttgccgacgggggccct
                                                                                                                                                                                                                                                                                                                                                                                                       aacagtattcatgctcatcgtatctgtgttggcactgataccagaaaccacaacattgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cttcagtgtgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaac 252
                                                                                                                                                                                                                                                                                                                    AGTTGGTGGAGGGGTG---GCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctatcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgc 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGGGAAGCCGAGCTGGGCGAGAAGTAGGGAAGGGCGGTGCTCCGCCGCGGTGCGG---G 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTCAGTGTGAAAGGCCACGTGAANATGCTGCGGCTGGATATTATCAACTCACTGGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGGGTCTGCAGACGCGATGGATAACG-GCAGCCGAAAATAAAACATCGCCCCTTNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  487;
zw67f10.s1 Soares_testis_NHT 3', mRNA sequence
                                   AA429945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shanghai Institute of Endocrinology, Rui-Jin Hospital 197 Rui-Jin II Road, Shanghai 200025, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 Guo Shoujing Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinese National Human Genome Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mbshi@ms.stn.sh.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB" 112 c 145 g 120 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pituitary tumor"
/dev_stage="Adult"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="TP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TPAAOA11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 8.7e-52;
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              Ното
                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                   441 aagttttgtaattttatattactttttagtttgatactaagtattaaacatatttctgta 500
                                                                       432 TCGCAGAACCTACTCAGGCAGCCAGCTGAGAAAGTTGAGGGAAAGTGCTGCTGCTGGGT 373
                                                                                          252 TCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCACAACATTGACAGTTGGTG
                                                                                                                                                                                                                                      261 tcatgctcatcgttatctgtgttggcactgataccagaaaaccaccaacattgacagttggtg
                                                                                                                                                                                                                                                                                                             201 tgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaacaacagtat 260
                                                                                                                                                                                                                                                                                                                                                                                     141 ctgcagacgcgatggataacgtgcagccgaaaataaaacatcgccccttctgcttcagtg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 tcgcagaacctactcaggcagccagctgagaagagttgagggaaagtgctgctgctgggt 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                 9a9999f9tttgcacttgtgacagcagtatgctgtcttgccgacggggcccttatttacc 380
                                                                                                                                                                                                                                                                                          TGAAAGGCCACGTGAAGATGCTGCGGCTGGATATTATCAACTCACTGGTAACAACAGTAT 253
                                                                                                                                                                                                                                                                                                                                                                 CTGCAGACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTG 313
AAGTTTTGTAATTTATATTACTTTTAGTTTGATACTAAGTATTAAACATATTTCTGTA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 432)

Hillier_L. Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie, T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997, Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -4lml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:781291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 430.4; DB 9
Pred. No. 1.9e-51;
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                                                                                                                                           367 CTGCAGACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTG
                                                                         141 ctgcagacgcgattggataacgtgcagccgaaaataaaacatcgccccttctgcttcagtg 200
201 tgaaaggccacgtgaagatgctgcggctggatattatcaactcactggtaacaacagtat 260
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                                                                                                                                                                                                                                                     427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov) for Seg primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine 4444 Forest park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3', mRNA sequence. AA455042
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                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                       were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.B. clones 260232-265223, 3404488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mixed (see below); Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site1: Not I; Site2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHHJ9W) were mixed, and se circles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:6043155"
/db_xref="taxon:9606"
/clone="IMAGE:812244"
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79.0%; Score 422; DB 9; 100.0%; Pred. No. 2.8e-50;

DB 9; Length 423;

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AI128804.1 GI:3597318
                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 423)
                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
           116
                                         NbHL19W."
                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                  same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                /sex="unknown"
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Best Local Similarity
Matches 422; Conserv
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